



## SEQUENCE LISTING

<110> DING, YOU  
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VINZANT, TODD B.  
DECKER, STEPHEN R.  
HIMMEL, MICHAEL E.

<120> THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS  
CELLULOLYTICUS

<130> 40170.6US01

<140> 09/917,783

<141> 2001-07-28

<160> 14

<170> PatentIn Ver. 2.1

<210> 1

<211> 1228

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of  
GuxA

<400> 1

Met Glu Arg Thr Gln Gln Ser Gly Arg Asn Cys Arg Tyr Gln Arg Gly  
1 5 10 15

Thr Thr Arg Met Pro Ala Ile Ser Lys Arg Leu Arg Ala Gly Val Leu  
20 25 30

Ala Gly Ala Val Ser Ile Ala Ala Ser Ile Val Pro Leu Ala Met Gln  
35 40 45

His Pro Ala Ile Ala Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala  
50 55 60

Thr Phe Phe Val Asn Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala  
65 70 75 80

Ala Asn Gln Thr Asn Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser  
85 90 95

Thr Tyr Ser Thr Ala Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly  
100 105 110

Val Asn Gly Gly Pro Gly Leu Thr Tyr Leu Asp Ala Ala Leu Ser  
115 120 125

Gln Gln Gln Gly Thr Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp  
130 135 140

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Leu Pro Gly Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Pro  
 145 150 155 160  
 Ala Thr Ala Ala Gly Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro  
 165 170 175  
 Ile Ala Ser Ile Leu Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val  
 180 185 190  
 Thr Ile Ile Glu Pro Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser  
 195 200 205  
 Ile Gln Ala Cys Ala Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu  
 210 215 220  
 Tyr Ala Leu Thr Lys Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met  
 225 230 235 240  
 Asp Ala Ala His Ser Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly  
 245 250 255  
 Tyr Val Gln Glu Val Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn  
 260 265 270  
 Gly Ile Asp Gly Phe Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys  
 275 280 285  
 Glu Pro Phe Met Thr Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu  
 290 295 300  
 Ser Ala Asn Phe Tyr Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr  
 305 310 315 320  
 Ala Val Asp Leu Tyr Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser  
 325 330 335  
 Ile Gly Met Leu Ile Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn  
 340 345 350  
 Glu Pro Thr Gly Pro Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn  
 355 360 365  
 Gln Ser Lys Ile Asp Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln  
 370 375 380  
 Asn Gly Ala Gly Leu Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe  
 385 390 395 400  
 Pro Asn Ala His Leu Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu  
 405 410 415  
 Ser Asp Gly Thr Ser Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser  
 420 425 430  
 Asp Pro Met Cys Asp Pro Thr Tyr Thr Thr Ser Tyr Gly Val Leu Thr  
 435 440 445

Asn Ala Leu Pro Asn Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln  
 450 455 460  
 Phe Asp Gln Leu Val Ala Asn Ala Arg Pro Ala Val Pro Thr Ser Thr  
 465 470 475 480  
 Ser Ser Ser Pro Pro Pro Pro Pro Ser Ala Ser Pro Ser  
 485 490 495  
 Pro Ser Pro Ser Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser  
 500 505 510  
 Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser  
 515 520 525  
 Ser Ser Pro Ser Pro Ser Pro Ser Ser Ser Pro Ser Pro Ser Pro Ser  
 530 535 540  
 Pro Ser Pro Ser Pro Ser Ser Ser Pro Ser Pro Ser Ser Ser Ser  
 545 550 555 560  
 Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser Ser Ser Pro Ser  
 565 570 575  
 Pro Ser Pro Thr Ser Ser Pro Val Ser Gly Gly Leu Lys Val Gln Tyr  
 580 585 590  
 Lys Asn Asn Asp Ser Ala Pro Gly Asp Asn Gln Ile Lys Pro Gly Leu  
 595 600 605  
 Gln Leu Val Asn Thr Gly Ser Ser Ser Val Asp Leu Ser Thr Val Thr  
 610 615 620  
 Val Arg Tyr Trp Phe Thr Arg Asp Gly Gly Ser Ser Thr Leu Val Tyr  
 625 630 635 640  
 Asn Cys Asp Trp Ala Ala Met Gly Cys Gly Asn Ile Arg Ala Ser Phe  
 645 650 655  
 Gly Ser Val Asn Pro Ala Thr Pro Thr Ala Asp Thr Tyr Leu Gln Leu  
 660 665 670  
 Ser Phe Thr Gly Gly Thr Leu Ala Ala Gly Gly Ser Thr Gly Glu Ile  
 675 680 685  
 Gln Asn Arg Val Asn Lys Ser Asp Trp Ser Asn Phe Thr Glu Thr Asn  
 690 695 700  
 Asp Tyr Ser Tyr Gly Thr Asn Thr Thr Phe Gln Asp Trp Thr Lys Val  
 705 710 715 720  
 Thr Val Tyr Val Asn Gly Val Leu Val Trp Gly Thr Glu Pro Ser Gly  
 725 730 735  
 Thr Ser Pro Ser Pro Thr Pro Ser Pro Ser Pro Ser Pro Ser Pro Ser  
 740 745 750

Pro Gly Gly Asp Val Thr Pro Pro Ser Val Pro Thr Gly Leu Val Val  
 755 760 765  
 Thr Gly Val Ser Gly Ser Ser Val Ser Leu Ala Trp Asn Ala Ser Thr  
 770 775 780  
 Asp Asn Val Gly Val Ala His Tyr Asn Val Tyr Arg Asn Gly Val Leu  
 785 790 795 800  
 Val Gly Gln Pro Thr Val Thr Ser Phe Thr Asp Thr Gly Leu Ala Ala  
 805 810 815  
 Gly Thr Ala Tyr Thr Tyr Thr Val Ala Ala Val Asp Ala Ala Gly Asn  
 820 825 830  
 Thr Ser Ala Pro Ser Thr Pro Val Thr Ala Thr Thr Thr Ser Pro Ser  
 835 840 845  
 Pro Ser Pro Thr Pro Thr Gly Thr Thr Val Thr Asp Cys Thr Pro Gly  
 850 855 860  
 Pro Asn Gln Asn Gly Val Thr Ser Val Gln Gly Asp Glu Tyr Arg Val  
 865 870 875 880  
 Gln Thr Asn Glu Trp Asn Ser Ser Ala Gln Gln Cys Leu Thr Ile Asn  
 885 890 895  
 Thr Ala Thr Gly Ala Trp Thr Val Ser Thr Ala Asn Phe Ser Gly Gly  
 900 905 910  
 Thr Gly Gly Ala Pro Ala Thr Tyr Pro Ser Ile Tyr Lys Gly Cys His  
 915 920 925  
 Trp Gly Asn Cys Thr Thr Lys Asn Val Gly Met Pro Ile Gln Ile Ser  
 930 935 940  
 Gln Ile Gly Ser Ala Val Thr Ser Trp Ser Thr Thr Gln Val Ser Ser  
 945 950 955 960  
 Gly Ala Tyr Asp Val Ala Tyr Asp Ile Trp Thr Asn Ser Thr Pro Thr  
 965 970 975  
 Thr Thr Gly Gln Pro Asn Gly Thr Glu Ile Met Ile Trp Leu Asn Ser  
 980 985 990  
 Arg Gly Gly Val Gln Pro Phe Gly Ser Gln Thr Ala Thr Gly Val Thr  
 995 1000 1005  
 Val Ala Gly His Thr Trp Asn Val Trp Gln Gly Gln Gln Thr Ser Trp  
 1010 1015 1020  
 Lys Ile Ile Ser Tyr Val Leu Thr Pro Gly Ala Thr Ser Ile Ser Asn  
 1025 1030 1035 1040  
 Leu Asp Leu Lys Ala Ile Phe Ala Asp Ala Ala Ala Arg Gly Ser Leu  
 1045 1050 1055

Asn Thr Ser Asp Tyr Leu Leu Asp Val Glu Ala Gly Phe Glu Ile Trp  
1060 1065 1070

Gln Gly Gly Gln Gly Leu Gly Ser Asn Ser Phe Ser Val Ser Val Thr  
1075 1080 1085

Ser Gly Thr Ser Ser Pro Thr Pro Ser Pro Ser Pro Thr Pro Thr Pro  
1090 1095 1100

Ser Pro Thr Pro Thr Pro Ser Pro Ser Pro Thr Pro Ser Pro Ser Pro  
1105 1110 1115 1120

Thr Ser Ser Pro Ser Ser Ser Gly Val Ala Cys Arg Ala Thr Tyr Val  
1125 1130 1135

Val Asn Ser Asp Trp Gly Ser Gly Phe Thr Ala Thr Val Thr Val Thr  
1140 1145 1150

Asn Thr Gly Ser Arg Ala Thr Asn Gly Trp Thr Val Ala Trp Ser Phe  
1155 1160 1165

Gly Gly Asn Gln Thr Val Thr Asn Tyr Trp Asn Thr Ala Leu Thr Gln  
1170 1175 1180

Ser Gly Ala Ser Val Thr Ala Thr Asn Leu Ser Tyr Asn Asn Val Ile  
1185 1190 1195 1200

Gln Pro Gly Gln Ser Thr Thr Phe Gly Phe Asn Gly Ser Tyr Ser Gly  
1205 1210 1215

Thr Asn Ala Ala Pro Thr Leu Ser Cys Thr Ala Ser  
1220 1225

<210> 2

<211> 3687

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of  
GuxA

<400> 2

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ccggccatct caaaacggct gcgagccggc gtctctgcgc gggcggtagag catcgacgcc 120  
tccatctgtc cgtctggcgt gcagcatcct gccatcgccg cgacgcacgt cgacaatccc 180  
tatgcccggag cgaccttctt ctctcaaccgc tactggggcg aagaagtaca gagcgaagcg 240  
gcgaaccaga ccaatgccac tctcgcagcg aaaatgcgcg tcgtttccac atattcgacg 300  
gccgtctgga tggaccgcat cgtctgcgac aacggcgctca acggcgggacc cggcttgacg 360  
acatatctgg acgcccgcct ctcccagcag cagggaacca cccctgaagt cattgagatt 420  
gtcatctacg atctgcgggg acgcgactgc gcggcgctcg cctccaaagg cgaactgccc 480  
tcgtacggcag cagggtttgca gacctatgaa acgcagtaca tcgatccgat tgcgagtatc 540  
ctgagcaatc cgaagtactc cagcctgcgg atcgtgacga tcattgagcc ggactcgctg 600  
ccaaacgcgg tcaccaatat gagcattcaa gcgtgtgcaa cggcgggtgcc gtattacgag 660  
caaggcatcg agtacgcgct cagcaaatgt cagcgcattc cgaacgtgta catctacatg 720  
gacgcgcgcc actccggctg gcttgggtgg cccaataatg ccagcgggata cgtacagaa 780  
gtccagaagg tcttcaacgc gagcatcggg gtcaacggca tcgacggctt cgtcaccac 840

acggcggaatt	acacgcccgtt	gaaggagccg	ttcatgaccc	ccaccacgca	ggtcggcgga	900
cagccggtgg	agtcggcgaa	ttctaccag	tggaaacctg	acatcgacga	agccgactac	960
gcgggtgact	tgtactcgcg	gctcgtcgcc	gctggcttct	caacgcagcat	ggcgatgctc	1020
atcgacacct	tacgaacccg	tgggggtgg	cgaacgaac	caacaggccc	gagcaccgcg	1080
accgatgtca	acaccttcgt	caaccagtcg	aagattgacc	ttcggcagca	ccggcgccgtg	1140
tgggtgcaac	agaacccgct	gggcctcgcc	cagcccgccg	aggcaagccc	ggcgacttcc	1200
ccgaacccgc	acctcgacgc	gtatgtctgg	atcaagccgc	cggtgagtc	ggacggcaca	1260
agcgctcgga	gcgatccgac	aactggcaag	aagtccgacc	ccatgtcgca	cccgactgac	1320
acgacgtcgt	acgggggtact	gaccaacccg	ttaccgaact	ccccgatcgc	cgggcagtgcc	1380
ttcccgccgc	agtttgacca	gcttgctcgc	aacgcacggc	cagcgtgccc	gacgtcgacc	1440
agctcgagcc	cgccgcctcc	gcgcgcaggt	ccgtcgctct	cgccgagtc	gagcccgagt	1500
ccgagcccca	gcagctcgcc	atccgctcgc	ccgtctccga	gctcgagccc	gtctccgtcg	1560
ccgagcccca	gtccgagccc	gagtagctcg	ccgtcgccgt	ctccgagctc	gagcccgctc	1620
ccgtcgccga	ccccgagtc	gagcccgagt	agctcgccgt	cgccgtctcc	gagctcgagc	1680
ccgtctccgt	gcggcagccc	gagtcgagc	ccgagtagct	cgccgtcgcc	gtctccgacg	1740
tcgtcgccga	tgtcgggtgg	gctgaaggtg	cagtaacaaga	acaatgatct	ggcgccgggtg	1800
gataaccaga	tcaaacccgg	ttccagattg	gtgaataccg	ggctcgctgc	gtgtgatttg	1860
tcgacgggtga	cggtgcccga	ctgggttcacc	cgggatgggtg	ggctcgctgc	actggtgtac	1920
aactgtgact	ggggcgccgt	gggggtgtggg	aatatcccg	ctcgtgtcgc	ctcggtgaac	1980
ccggcgacgc	cgacggcgga	cacctacctg	cagttgtcgt	tcactgggtg	aacgttggcc	2040
gctggtggctg	cgacgggtga	gattcaaaac	cgggtgaata	agagtgactg	gtcgaatttc	2100
accgagacca	atgactactc	gtatgggagc	aacaccacct	tccaggagtc	gacgaaggtg	2160
accggtgtac	tcaacggcgt	gttgggtgtg	gggactgaac	cgctccggc	cagccccagc	2220
cccaaccatg	ccccgagccc	gagcccgagc	ccgagcccg	gtggggatgt	gacgcgcccg	2280
agtggtccga	ccggcttggg	ggtagcgggg	gtgagtggtg	cgctcggtgc	gttggcgctg	2340
aatgcgtcga	cggtatacgt	gggggtggcg	cattacaacg	tgtagccgaa	cggggtgttg	2400
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accgccacca	ccacgcgctc	cagccccagc	cccacgcgga	cggggacac	ggtcaccgac	2580
tgacgcgccg	gtctctaacca	gaatgggtg	accagcgctg	agggcgacga	ataccgggtg	2640
cagaccaatg	agtggaattc	gtcgccccag	cagtgccctca	ccatcaatc	cgcgaccggg	2700
gcctggacgc	tgagcaactg	gaacttcagc	ggtgggacgc	cggtgcgccc	cgcgacgtat	2760
ccgtggacgc	acaaggccgtg	ccaactggggc	aactgcacca	cgaagaacgt	cgggatgccc	2820
atccagatca	gtcagatttg	ttcggctgtg	acgtcgtgga	gtacgacgca	ggtgtcgtcg	2880
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tcgcagacag	cgacgggtgtg	cagcgtcgtc	ggtaacacgt	ggaatgtctg	gcaggcgacg	3060
catgacctcgt	ggaagattat	ttcctaactc	ctgacccccg	gtcgacgtc	gatcagtaat	3120
ctggatttga	agggcatttt	cgcggacgccc	gcggcacgcg	ggtcgctcaa	gactcccgat	3180
taacctgtcg	acgttgaggg	cggggttgag	atctggcagg	gtgggtcagg	cctggggcagc	3240
aactcgttca	gcgtctccgt	gacgagcgcc	acgtccagcc	cgacacccag	cccgagccgc	3300
acgcccagac	cgaagcccg	gcgcacacgc	ttccgagccc	cgaacccgctc	gcgagctccg	3360
accagctcgc	cgctcgtcgt	gggtgtggcg	tgccgggcga	cgtatgtggt	gaatagtgat	3420
tgggggtctg	ggtttacggc	cagcgtgacg	gtgacgaata	ggcgagccgc	ggcgagcga	3480
gggtggagcg	tggcgtgtgc	gtttgggtgg	aatcagacgg	tcacgaacta	ctggaaacat	3540
cggttgaccc	aatcaggtgc	atcgttgacg	gcgacgaacc	tgagttacaa	caactgtgatc	3600
caaccgggtc	agtcgacac	cttcggattc	aacggaagtt	actcaggaac	aaacgcgcgc	3660
ccgacgctca	gctgcacacg	cagctga				3687

<210> 3  
 <211> 53  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Segment of  
 GuxA

&lt;400&gt; 3

Met Glu Arg Thr Gln Gln Ser Gly Arg Asn Cys Arg Tyr Gln Arg Gly  
 1 5 10 15

Thr Thr Arg Met Pro Ala Ile Ser Lys Arg Leu Arg Ala Gly Val Leu  
 20 25 30

Ala Gly Ala Val Ser Ile Ala Ala Ser Ile Val Pro Leu Ala Met Gln  
 35 40 45

His Pro Ala Ile Ala  
 50

&lt;210&gt; 4

&lt;211&gt; 423

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Segment of  
 GuxA

&lt;400&gt; 4

Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala Thr Phe Phe Val Asn  
 1 5 10 15

Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala Ala Asn Gln Thr Asn  
 20 25 30

Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser Thr Tyr Ser Thr Ala  
 35 40 45

Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly Val Asn Gly Gly Pro  
 50 55 60

Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser Gln Gln Gln Gly Thr  
 65 70 75 80

Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp Leu Pro Gly Arg Asp  
 85 90 95

Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Pro Ala Thr Ala Ala Gly  
 100 105 110

Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro Ile Ala Ser Ile Leu  
 115 120 125

Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val Thr Ile Ile Glu Pro  
 130 135 140

Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser Ile Gln Ala Cys Ala  
 145 150 155 160

Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu Tyr Ala Leu Thr Lys  
 165 170 175

Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met Asp Ala Ala His Ser  
 180 185 190  
 Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly Tyr Val Gln Glu Val  
 195 200 205  
 Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn Gly Ile Asp Gly Phe  
 210 215 220  
 Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys Glu Pro Phe Met Thr  
 225 230 235 240  
 Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu Ser Ala Asn Phe Tyr  
 245 250 255  
 Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr Ala Val Asp Leu Tyr  
 260 265 270  
 Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser Ile Gly Met Leu Ile  
 275 280 285  
 Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn Glu Pro Thr Gly Pro  
 290 295 300  
 Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn Gln Ser Lys Ile Asp  
 305 310 315 320  
 Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln Asn Gly Ala Gly Leu  
 325 330 335  
 Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe Pro Asn Ala His Leu  
 340 345 350  
 Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu Ser Asp Gly Thr Ser  
 355 360 365  
 Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser Asp Pro Met Cys Asp  
 370 375 380  
 Pro Thr Tyr Thr Thr Ser Tyr Gly Val Leu Thr Asn Ala Leu Pro Asn  
 385 390 395 400  
 Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln Phe Asp Gln Leu Val  
 405 410 415  
 Ala Asn Ala Arg Pro Ala Val  
 420

<210> 5  
 <211> 150  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Segment of  
 GuxA



<400> 5  
 Val Ser Gly Gly Leu Lys Val Gln Tyr Lys Asn Asn Asp Ser Ala Pro  
 1 5 10 15  
 Gly Asp Asn Gln Ile Lys Pro Gly Leu Gln Leu Val Asn Thr Gly Ser  
 20 25 30  
 Ser Ser Val Asp Leu Ser Thr Val Thr Val Arg Tyr Trp Phe Thr Arg  
 35 40 45  
 Asp Gly Gly Ser Ser Thr Leu Val Tyr Asn Cys Asp Trp Ala Ala Met  
 50 55 60  
 Gly Cys Gly Asn Ile Arg Ala Ser Phe Gly Ser Val Asn Pro Ala Thr  
 65 70 75 80  
 Pro Thr Ala Asp Thr Tyr Leu Gln Leu Ser Phe Thr Gly Gly Thr Leu  
 85 90 95  
 Ala Ala Gly Gly Ser Thr Gly Glu Ile Gln Asn Arg Val Asn Lys Ser  
 100 105 110  
 Asp Trp Ser Asn Phe Thr Glu Thr Asn Asp Tyr Ser Tyr Gly Thr Asn  
 115 120 125  
 Thr Thr Phe Gln Asp Trp Thr Lys Val Thr Val Tyr Val Asn Gly Val  
 130 135 140  
 Leu Val Trp Gly Thr Glu  
 145 150

<210> 6  
 <211> 1043  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Segment of  
 GuxA

<400> 6  
 Met Glu Arg Thr Gln Gln Ser Gly Arg Asn Cys Arg Tyr Gln Arg Gly  
 1 5 10 15  
 Thr Thr Arg Met Pro Ala Ile Ser Lys Arg Leu Arg Ala Gly Val Leu  
 20 25 30  
 Ala Gly Ala Val Ser Ile Ala Ala Ser Ile Val Pro Leu Ala Met Gln  
 35 40 45  
 His Pro Ala Ile Ala Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala  
 50 55 60  
 Thr Phe Phe Val Asn Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala  
 65 70 75 80

Ala Asn Gln Thr Asn Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser  
85 90 95

Thr Tyr Ser Thr Ala Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly  
100 105 110

Val Asn Gly Gly Pro Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser  
115 120 125

Gln Gln Gln Gly Thr Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp  
130 135 140

Leu Pro Gly Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Pro  
145 150 155 160

Ala Thr Ala Ala Gly Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro  
165 170 175

Ile Ala Ser Ile Leu Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val  
180 185 190

Thr Ile Ile Glu Pro Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser  
195 200 205

Ile Gln Ala Cys Ala Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu  
210 215 220

Tyr Ala Leu Thr Lys Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met  
225 230 235 240

Asp Ala Ala His Ser Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly  
245 250 255

Tyr Val Gln Glu Val Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn  
260 265 270

Gly Ile Asp Gly Phe Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys  
275 280 285

Glu Pro Phe Met Thr Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu  
290 295 300

Ser Ala Asn Phe Tyr Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr  
305 310 315 320

Ala Val Asp Leu Tyr Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser  
325 330 335

Ile Gly Met Leu Ile Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn  
340 345 350

Glu Pro Thr Gly Pro Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn  
355 360 365

Gln Ser Lys Ile Asp Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln  
370 375 380

Asn Gly Ala Gly Leu Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe  
 385 390 395 400  
 Pro Asn Ala His Leu Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu  
 405 410 415  
 Ser Asp Gly Thr Ser Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser  
 420 425 430  
 Asp Pro Met Cys Asp Pro Thr Tyr Thr Thr Ser Tyr Gly Val Leu Thr  
 435 440 445  
 Asn Ala Leu Pro Asn Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln  
 450 455 460  
 Phe Asp Gln Leu Val Ala Asn Ala Arg Pro Ala Val Val Ser Gly Gly  
 465 470 475 480  
 Leu Lys Val Gln Tyr Lys Asn Asn Asp Ser Ala Pro Gly Asp Asn Gln  
 485 490 495  
 Ile Lys Pro Gly Leu Gln Leu Val Asn Thr Gly Ser Ser Ser Val Asp  
 500 505 510  
 Leu Ser Thr Val Thr Val Arg Tyr Trp Phe Thr Arg Asp Gly Gly Ser  
 515 520 525  
 Ser Thr Leu Val Tyr Asn Cys Asp Trp Ala Ala Met Gly Cys Gly Asn  
 530 535 540  
 Ile Arg Ala Ser Phe Gly Ser Val Asn Pro Ala Thr Pro Thr Ala Asp  
 545 550 555 560  
 Thr Tyr Leu Gln Leu Ser Phe Thr Gly Gly Thr Leu Ala Ala Gly Gly  
 565 570 575  
 Ser Thr Gly Glu Ile Gln Asn Arg Val Asn Lys Ser Asp Trp Ser Asn  
 580 585 590  
 Phe Thr Glu Thr Asn Asp Tyr Ser Tyr Gly Thr Asn Thr Thr Phe Gln  
 595 600 605  
 Asp Trp Thr Lys Val Thr Val Tyr Val Asn Gly Val Leu Val Trp Gly  
 610 615 620  
 Thr Glu Asp Val Thr Pro Pro Ser Val Pro Thr Gly Leu Val Val Thr  
 625 630 635 640  
 Gly Val Ser Gly Ser Ser Val Ser Leu Ala Trp Asn Ala Ser Thr Asp  
 645 650 655  
 Asn Val Gly Val Ala His Tyr Asn Val Tyr Arg Asn Gly Val Leu Val  
 660 665 670  
 Gly Gln Pro Thr Val Thr Ser Phe Thr Asp Thr Gly Leu Ala Ala Gly  
 675 680 685

Thr Ala Tyr Thr Tyr Thr Val Ala Ala Val Asp Ala Ala Gly Asn Thr  
 690 695 700  
 Ser Ala Pro Ser Thr Pro Val Asp Cys Thr Pro Gly Pro Asn Gln Asn  
 705 710 715 720  
 Gly Val Thr Ser Val Gln Asp Gly Glu Tyr Arg Val Gln Thr Asn Glu  
 725 730 735  
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 Ala Trp Thr Val Ser Thr Ala Asn Phe Ser Gly Gly Thr Gly Gly Ala  
 755 760 765  
 Pro Ala Thr Tyr Pro Ser Ile Tyr Lys Gly Cys His Trp Gly Asn Cys  
 770 775 780  
 Thr Thr Lys Asn Val Gly Met Pro Ile Gln Ile Ser Gln Ile Gly Ser  
 785 790 795 800  
 Ala Val Thr Ser Trp Ser Thr Thr Gln Val Ser Ser Gly Ala Tyr Asp  
 805 810 815  
 Val Ala Tyr Asp Ile Trp Thr Asn Ser Thr Pro Thr Thr Gly Gln  
 820 825 830  
 Pro Asn Gly Thr Glu Ile Met Ile Trp Leu Asn Ser Arg Gly Gly Val  
 835 840 845  
 Gln Pro Phe Gly Ser Gln Thr Ala Thr Gly Val Thr Val Ala Gly His  
 850 855 860  
 Thr Trp Asn Val Trp Gln Gly Gln Gln Thr Ser Trp Lys Ile Ile Ser  
 865 870 875 880  
 Tyr Val Leu Thr Pro Gly Ala Thr Ser Ile Ser Asn Leu Asp Leu Lys  
 885 890 895  
 Ala Ile Phe Ala Asp Ala Ala Ala Arg Gly Ser Leu Asn Thr Ser Asp  
 900 905 910  
 Tyr Leu Leu Asp Val Glu Ala Gly Phe Glu Ile Trp Gln Gly Gly Gln  
 915 920 925  
 Gly Leu Gly Ser Asn Ser Phe Ser Val Ser Val Thr Ser Gly Gly Val  
 930 935 940  
 Ala Cys Arg Ala Thr Tyr Val Val Asn Ser Asp Trp Gly Ser Gly Phe  
 945 950 955 960  
 Thr Ala Thr Val Thr Val Thr Asn Thr Gly Ser Arg Ala Thr Asn Gly  
 965 970 975  
 Trp Thr Val Ala Trp Ser Phe Gly Gly Asn Gln Thr Val Thr Asn Tyr  
 980 985 990

Trp Asn Thr Ala Leu Thr Gln Ser Gly Ala Ser Val Thr Ala Thr Asn  
995 1000 1005

Leu Tyr Ser Asn Asn Val Ile Gln Pro Gly Gln Ser Thr Thr Phe Gly  
1010 1015 1020

Phe Asn Gly Ser Tyr Ser Gly Thr Asn Ala Ala Pro Thr Leu Ser Cys  
1025 1030 1035 1040

Thr Ala Ser

<210> 7

<211> 231

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of  
GuxA

<400> 7

Asp Cys Thr Pro Gly Pro Asn Gln Asn Gly Val Thr Ser Val Gln Asp  
1 5 10 15

Gly Glu Tyr Arg Val Gln Thr Asn Glu Trp Asn Ser Ser Ala Gln Gln  
20 25 30

Cys Leu Thr Ile Asn Thr Ala Thr Gly Ala Trp Thr Val Ser Thr Ala  
35 40 45

Asn Phe Ser Gly Gly Thr Gly Gly Ala Pro Ala Thr Tyr Pro Ser Ile  
50 55 60

Tyr Lys Gly Cys His Trp Gly Asn Cys Thr Thr Lys Asn Val Gly Met  
65 70 75 80

Pro Ile Gln Ile Ser Gln Ile Gly Ser Ala Val Thr Ser Trp Ser Thr  
85 90 95

Thr Gln Val Ser Ser Gly Ala Tyr Asp Val Ala Tyr Asp Ile Trp Thr  
100 105 110

Asn Ser Thr Pro Thr Thr Thr Gly Gln Pro Asn Gly Thr Glu Ile Met  
115 120 125

Ile Trp Leu Asn Ser Arg Gly Gly Val Gln Pro Phe Gly Ser Gln Thr  
130 135 140

Ala Thr Gly Val Thr Val Ala Gly His Thr Trp Asn Val Trp Gln Gly  
145 150 155 160

Gln Gln Thr Ser Trp Lys Ile Ile Ser Tyr Val Leu Thr Pro Gly Ala  
165 170 175

Thr Ser Ile Ser Asn Leu Asp Leu Lys Ala Ile Phe Ala Asp Ala Ala  
180 185 190

Ala Arg Gly Ser Leu Asn Thr Ser Asp Tyr Leu Leu Asp Val Glu Ala  
195 200 205

Gly Phe Glu Ile Trp Gln Gly Gly Gln Gly Leu Gly Ser Asn Ser Phe  
210 215 220

Ser Val Ser Val Thr Ser Gly  
225 230

<210> 8

<211> 101

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Segment of  
GuxA

<400> 8

Gly Val Ala Cys Arg Ala Thr Tyr Val Val Asn Ser Asp Trp Gly Ser  
1 5 10 15

Gly Phe Thr Ala Thr Val Thr Val Thr Asn Thr Gly Ser Arg Ala Thr  
20 25 30

Asn Gly Trp Thr Val Ala Trp Ser Phe Gly Gly Asn Gln Thr Val Thr  
35 40 45

Asn Tyr Trp Asn Thr Ala Leu Thr Gln Ser Gly Ala Ser Val Thr Ala  
50 55 60

Thr Asn Leu Tyr Ser Asn Asn Val Ile Gln Pro Gly Gln Ser Thr Thr  
65 70 75 80

Phe Gly Phe Asn Gly Ser Tyr Ser Gly Thr Asn Ala Ala Pro Thr Leu  
85 90 95

Ser Cys Thr Ala Ser  
100

<210> 9

<211> 423

<212> PRT

<213> Acidothermus cellulolyticus

<400> 9

Ala Thr His Val Asp Asn Pro Tyr Ala Gly Ala Thr Phe Phe Val Asn  
1 5 10 15

Pro Tyr Trp Ala Gln Glu Val Gln Ser Glu Ala Ala Asn Gln Thr Asn  
20 25 30

Ala Thr Leu Ala Ala Lys Met Arg Val Val Ser Thr Tyr Ser Thr Ala  
35 40 45

Val Trp Met Asp Arg Ile Ala Ala Ile Asn Gly Val Asn Gly Gly Pro  
 50 55 60  
 Gly Leu Thr Thr Tyr Leu Asp Ala Ala Leu Ser Gln Gln Gln Gly Thr  
 65 70 75 80  
 Thr Pro Glu Val Ile Glu Ile Val Ile Tyr Asp Leu Pro Gly Arg Asp  
 85 90 95  
 Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Pro Ala Thr Ala Ala Gly  
 100 105 110  
 Leu Gln Thr Tyr Glu Thr Gln Tyr Ile Asp Pro Ile Ala Ser Ile Leu  
 115 120 125  
 Ser Asn Pro Lys Tyr Ser Ser Leu Arg Ile Val Thr Ile Ile Glu Pro  
 130 135 140  
 Asp Ser Leu Pro Asn Ala Val Thr Asn Met Ser Ile Gln Ala Cys Ala  
 145 150 155 160  
 Thr Ala Val Pro Tyr Tyr Glu Gln Gly Ile Glu Tyr Ala Leu Thr Lys  
 165 170 175  
 Leu His Ala Ile Pro Asn Val Tyr Ile Tyr Met Asp Ala Ala His Ser  
 180 185 190  
 Gly Trp Leu Gly Trp Pro Asn Asn Ala Ser Gly Tyr Val Gln Glu Val  
 195 200 205  
 Gln Lys Val Leu Asn Ala Ser Ile Gly Val Asn Gly Ile Asp Gly Phe  
 210 215 220  
 Val Thr Asn Thr Ala Asn Tyr Thr Pro Leu Lys Glu Pro Phe Met Thr  
 225 230 235 240  
 Ala Thr Gln Gln Val Gly Gly Gln Pro Val Glu Ser Ala Asn Phe Tyr  
 245 250 255  
 Gln Trp Asn Pro Asp Ile Asp Glu Ala Asp Tyr Ala Val Asp Leu Tyr  
 260 265 270  
 Ser Arg Leu Val Ala Ala Gly Phe Pro Ser Ser Ile Gly Met Leu Ile  
 275 280 285  
 Asp Thr Leu Arg Asn Gly Trp Gly Gly Pro Asn Glu Pro Thr Gly Pro  
 290 295 300  
 Ser Thr Ala Thr Asp Val Asn Thr Phe Val Asn Gln Ser Lys Ile Asp  
 305 310 315 320  
 Leu Arg Gln His Arg Gly Leu Trp Cys Asn Gln Asn Gly Ala Gly Leu  
 325 330 335  
 Gly Gln Pro Pro Gln Ala Ser Pro Thr Asp Phe Pro Asn Ala His Leu  
 340 345 350

Asp Ala Tyr Val Trp Ile Lys Pro Pro Gly Glu Ser Asp Gly Thr Ser  
355 360 365

Ala Ala Ser Asp Pro Thr Thr Gly Lys Lys Ser Asp Pro Met Cys Asp  
370 375 380

Pro Thr Tyr Thr Thr Ser Tyr Gly Val Leu Thr Asn Ala Leu Pro Asn  
385 390 395 400

Ser Pro Ile Ala Gly Gln Trp Phe Pro Ala Gln Phe Asp Gln Leu Val  
405 410 415

Ala Asn Ala Arg Pro Ala Val  
420

<210> 10

<211> 430

<212> PRT

<213> Cellulomonas fimi

<400> 10

Ala Pro Val His Val Asp Asn Pro Tyr Ala Gly Ala Val Gln Tyr Val  
1 5 10 15

Asn Pro Thr Trp Ala Ala Ser Val Asn Ala Ala Ala Gly Arg Gln Ser  
20 25 30

Ala Asp Pro Ala Leu Ala Ala Lys Met Arg Thr Val Ala Gly Gln Pro  
35 40 45

Thr Ala Val Trp Met Asp Arg Ile Ser Ala Ile Thr Gly Asn Ala Asp  
50 55 60

Gly Asn Gly Leu Lys Phe His Leu Asp Asn Ala Val Ala Gln Gln Lys  
65 70 75 80

Ala Ala Gly Val Pro Leu Val Phe Asn Leu Val Ile Tyr Asp Leu Pro  
85 90 95

Gly Arg Asp Cys Phe Ala Leu Ala Ser Asn Gly Glu Leu Pro Ala Thr  
100 105 110

Asp Ala Gly Leu Ala Arg Tyr Lys Ser Glu Tyr Ile Asp Pro Ile Ala  
115 120 125

Asp Leu Leu Asp Asn Pro Glu Tyr Glu Ser Ile Arg Ile Ala Ala Thr  
130 135 140

Ile Glu Pro Asp Ser Leu Pro Asn Leu Thr Thr Asn Ile Ser Glu Pro  
145 150 155 160

Ala Cys Gln Gln Ala Ala Pro Tyr Tyr Arg Gln Gly Val Lys Tyr Ala  
165 170 175

Leu Asp Lys Leu His Ala Ile Pro Asn Val Tyr Asn Tyr Ile Asp Ile  
180 185 190



Gly His Ser Gly Trp Leu Gly Trp Asp Ser Asn Ala Gly Pro Ser Ala  
195 200 205

Thr Leu Phe Ala Glu Val Ala Lys Ser Thr Thr Ala Gly Phe Ala Ser  
210 215 220

Ile Asp Gly Phe Val Ser Asp Val Ala Asn Thr Thr Pro Leu Glu Glu  
225 230 235 240

Pro Leu Leu Ser Asp Ser Ser Leu Thr Ile Asn Asn Thr Pro Ile Arg  
245 250 255

Ser Ser Lys Phe Tyr Glu Trp Asn Phe Asp Phe Asp Glu Ile Asp Tyr  
260 265 270

Thr Ala His Met His Arg Leu Leu Val Ala Ala Gly Phe Pro Ser Ser  
275 280 285

Ile Gly Met Leu Val Asp Thr Ser Arg Asn Gly Trp Gly Gly Pro Asn  
290 295 300

Arg Pro Thr Ser Ile Thr Ala Ser Thr Asp Val Asn Ala Tyr Val Asp  
305 310 315 320

Ala Asn Arg Val Asp Arg Arg Val His Arg Gly Ala Trp Cys Asn Pro  
325 330 335

Leu Gly Ala Gly Ile Gly Arg Phe Pro Glu Ala Thr Pro Ser Gly Tyr  
340 345 350

Ala Ala Ser His Leu Asp Ala Phe Val Trp Ile Lys Pro Pro Gly Glu  
355 360 365

Ser Asp Gly Ala Ser Thr Asp Ile Pro Asn Asp Gln Gly Lys Arg Phe  
370 375 380

Asp Arg Met Cys Asp Pro Thr Phe Val Ser Pro Lys Leu Asn Asn Gln  
385 390 395 400

Leu Thr Gly Ala Thr Pro Asn Ala Pro Leu Ala Gly Gln Trp Phe Glu  
405 410 415

Glu Gln Phe Val Thr Leu Val Lys Asn Ala Tyr Pro Val Ile  
420 425 430

<210> 11

<211> 432

<212> PRT

<213> Thermobifida fusca

<400> 11

Pro Gly Gly Pro Thr Asn Pro Pro Thr Asn Pro Gly Glu Lys Val Asp  
1 5 10 15

Asn Pro Phe Glu Gly Ala Lys Leu Tyr Val Asn Pro Val Trp Ser Ala  
20 25 30

Lys Ala Ala Glu Pro Gly Gly Ser Ala Val Ala Asn Glu Ser Thr  
 35 40 45  
 Ala Val Trp Leu Asp Arg Ile Gly Ala Ile Glu Gly Asn Asp Ser Pro  
 50 55 60  
 Thr Thr Gly Ser Met Gly Leu Arg Asp His Leu Glu Glu Ala Val Arg  
 65 70 75 80  
 Gln Ser Gly Gly Asp Pro Leu Thr Ile Gln Val Val Ile Tyr Asn Leu  
 85 90 95  
 Pro Gly Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Leu Gly Pro  
 100 105 110  
 Asp Glu Leu Asp Arg Tyr Lys Ser Glu Tyr Ile Asp Pro Ile Ala Asp  
 115 120 125  
 Ile Met Trp Asp Phe Ala Asp Tyr Glu Asn Leu Arg Ile Val Ala Ile  
 130 135 140  
 Ile Glu Ile Asp Ser Leu Pro Asn Leu Val Thr Asn Val Gly Gly Asn  
 145 150 155 160  
 Gly Gly Thr Glu Leu Cys Ala Tyr Met Lys Gln Asn Gly Gly Tyr Val  
 165 170 175  
 Asn Gly Val Gly Tyr Ala Leu Arg Lys Leu Gly Glu Ile Pro Asn Val  
 180 185 190  
 Tyr Asn Tyr Ile Asp Ala Ala His His Gly Trp Ile Gly Trp Asp Ser  
 195 200 205  
 Asn Phe Gly Pro Ser Val Asp Ile Phe Tyr Glu Ala Ala Asn Ala Ser  
 210 215 220  
 Gly Ser Thr Val Asp Tyr Val His Gly Phe Ile Ser Asn Thr Ala Asn  
 225 230 235 240  
 Tyr Ser Ala Thr Val Glu Pro Tyr Leu Asp Val Asn Gly Thr Val Asn  
 245 250 255  
 Gly Gln Leu Ile Arg Gln Ser Lys Trp Val Asp Trp Asn Gln Tyr Val  
 260 265 270  
 Asp Glu Leu Ser Phe Val Gln Asp Leu Arg Gln Ala Leu Ile Ala Lys  
 275 280 285  
 Gly Phe Arg Ser Asp Ile Gly Met Leu Ile Asp Thr Ser Arg Asn Gly  
 290 295 300  
 Trp Gly Gly Pro Asn Arg Pro Thr Gly Pro Ser Ser Ser Thr Asp Leu  
 305 310 315 320  
 Asn Thr Tyr Val Asp Glu Ser Arg Ile Asp Arg Arg Ile His Pro Gly  
 325 330 335

Asn Trp Cys Asn Gln Ala Gly Ala Gly Leu Gly Glu Arg Pro Thr Val  
 340 345 350

Asn Pro Ala Pro Gly Val Asp Ala Tyr Val Trp Val Lys Pro Pro Gly  
 355 360 365

Glu Ser Asp Gly Ala Ser Glu Glu Ile Pro Asn Asp Glu Gly Lys Gly  
 370 375 380

Phe Asp Arg Met Cys Asp Pro Thr Tyr Gln Gly Asn Ala Arg Asn Gly  
 385 390 395 400

Asn Asn Pro Ser Gly Ala Leu Pro Asn Ala Pro Ile Ser Gly His Trp  
 405 410 415

Phe Ser Ala Gln Phe Arg Glu Leu Leu Ala Asn Ala Tyr Pro Pro Leu  
 420 425 430

<210> 12  
 <211> 221  
 <212> PRT  
 <213> Acidothermus cellulolyticus

<400> 12  
 Asn Gln Gln Ile Cys Asp Arg Tyr Gly Thr Thr Thr Ile Gln Asp Arg  
 1 5 10 15

Tyr Val Val Gln Asn Asn Arg Trp Gly Thr Ser Ala Thr Gln Cys Ile  
 20 25 30

Asn Val Thr Gly Asn Gly Phe Glu Ile Thr Gln Ala Asp Gly Ser Val  
 35 40 45

Pro Thr Asn Gly Ala Pro Lys Ser Tyr Pro Ser Val Tyr Asp Gly Cys  
 50 55 60

His Tyr Gly Asn Cys Ala Pro Arg Thr Thr Leu Pro Met Arg Ile Ser  
 65 70 75 80

Ser Ile Gly Ser Ala Pro Ser Ser Val Ser Tyr Arg Tyr Thr Gly Asn  
 85 90 95

Gly Val Tyr Asn Ala Ala Tyr Asp Ile Trp Leu Asp Pro Thr Pro Arg  
 100 105 110

Thr Asn Gly Val Asn Arg Thr Glu Ile Met Ile Trp Phe Asn Arg Val  
 115 120 125

Gly Pro Val Gln Pro Ile Gly Ser Pro Val Gly Thr Ala His Val Gly  
 130 135 140

Gly Arg Ser Trp Glu Val Trp Thr Gly Ser Asn Gly Ser Asn Asp Val  
 145 150 155 160

Ile Ser Phe Leu Ala Pro Ser Ala Ile Ser Ser Trp Ser Phe Asp Val  
 165 170 175  
 Lys Asp Phe Val Asp Gln Ala Val Ser His Gly Leu Ala Thr Pro Asp  
 180 185 190  
 Trp Tyr Leu Thr Ser Ile Gln Ala Gly Phe Glu Pro Trp Glu Gly Gly  
 195 200 205  
 Thr Gly Leu Ala Val Asn Ser Phe Ser Ser Ala Val Asn  
 210 215 220

<210> 13  
 <211> 221  
 <212> PRT  
 <213> Streptomyces sp.

<400> 13  
 Asp Thr Thr Ile Cys Glu Pro Phe Gly Thr Thr Thr Ile Gln Gly Arg  
 1 5 10 15  
 Tyr Val Val Gln Asn Asn Arg Trp Gly Ser Thr Ala Pro Gln Cys Val  
 20 25 30  
 Thr Ala Thr Asp Thr Gly Phe Arg Val Thr Gln Ala Asp Gly Ser Ala  
 35 40 45  
 Pro Thr Asn Gly Ala Pro Lys Ser Tyr Pro Ser Val Phe Asn Gly Cys  
 50 55 60  
 His Tyr Thr Asn Cys Ser Pro Gly Thr Asp Leu Pro Val Arg Leu Asp  
 65 70 75 80  
 Thr Val Ser Ala Ala Pro Ser Ser Ile Ser Tyr Gly Phe Val Asp Gly  
 85 90 95  
 Ala Val Tyr Asn Ala Ser Tyr Asp Ile Trp Leu Asp Pro Thr Ala Arg  
 100 105 110  
 Thr Asp Gly Val Asn Gln Thr Glu Ile Met Ile Trp Phe Asn Arg Val  
 115 120 125  
 Gly Pro Ile Gln Pro Ile Gly Ser Pro Val Gly Thr Ala Ser Val Gly  
 130 135 140  
 Gly Arg Thr Trp Glu Val Trp Ser Gly Gly Asn Gly Ser Asn Asp Val  
 145 150 155 160  
 Leu Ser Phe Val Ala Pro Ser Ala Ile Ser Gly Trp Ser Phe Asp Val  
 165 170 175  
 Met Asp Phe Val Arg Ala Thr Val Ala Arg Gly Leu Ala Glu Asn Asp  
 180 185 190  
 Trp Tyr Leu Thr Ser Val Gln Ala Gly Phe Glu Pro Trp Gln Asn Gly  
 195 200 205

Ala Gly Leu Ala Val Asn Ser Phe Ser Ser Thr Val Glu  
 210 215 220

<210> 14  
 <211> 228  
 <212> PRT  
 <213> Streptomyces lividans

<400> 14  
 Cys Thr Pro Gly Pro Asn Gln Asn Gly Val Thr Ser Val Gln Gly Asp  
 1 5 10 15

Glu Tyr Arg Val Gln Thr Asn Glu Trp Asn Ser Ser Ala Gln Gln Cys  
 20 25 30

Leu Thr Ile Asn Thr Ala Thr Gly Ala Trp Thr Val Ser Thr Ala Asn  
 35 40 45

Phe Ser Gly Gly Thr Gly Gly Ala Pro Ala Thr Tyr Pro Ser Ile Tyr  
 50 55 60

Lys Gly Cys His Trp Gly Asn Cys Thr Thr Lys Asn Val Gly Met Pro  
 65 70 75 80

Ile Gln Ile Ser Gln Ile Gly Ser Ala Val Thr Ser Trp Ser Thr Thr  
 85 90 95

Gln Val Ser Ser Gly Ala Tyr Asp Val Ala Tyr Asp Ile Trp Thr Asn  
 100 105 110

Ser Thr Pro Thr Thr Thr Gly Gln Pro Asn Gly Thr Glu Ile Met Ile  
 115 120 125

Trp Leu Asn Ser Arg Gly Gly Val Gln Pro Phe Gly Ser Gln Thr Ala  
 130 135 140

Thr Gly Val Thr Val Ala Gly His Thr Trp Asn Val Trp Gln Gly Gln  
 145 150 155 160

Gln Thr Ser Trp Lys Ile Ile Ser Tyr Val Leu Thr Pro Gly Ala Thr  
 165 170 175

Ser Ile Ser Asn Leu Asp Leu Lys Ala Ile Phe Ala Asp Ala Ala Ala  
 180 185 190

Arg Gly Ser Leu Asn Thr Ser Asp Tyr Leu Leu Asp Val Glu Ala Gly  
 195 200 205

Phe Glu Ile Trp Gln Gly Gly Gln Gly Leu Gly Ser Asn Ser Phe Ser  
 210 215 220

Val Ser Val Thr  
 225